

WE CLAIM:

1. A process for identifying specific members of a previously unknown protein-ligand binding pair, comprising the steps of:
 - 5 (a) synthesizing a ligand library onto resin beads to form an immobilized ligand library, wherein each bead of the immobilized library comprises one member of the ligand library;
 - (b) incubating the immobilized ligand library with two or more differentially labeled protein mixtures;
 - 10 (c) detecting an immobilized ligand-protein binding pair from the incubation mixture;
 - (d) identifying the ligand of the specific ligand-binding pair; and
 - (e) identifying the protein of the ligand-protein binding pair,wherein the identified ligand and protein are specific members of a previously unknown differential ligand-protein binding pair.
- 15 2. A process for identifying specific members of a previously unknown protein-ligand binding pair, comprising the steps of:
 - (a) synthesizing a ligand library onto resin beads comprising polyethylene glycol to form an immobilized ligand library, wherein each bead of the immobilized li-
20 brary comprises one member of the ligand library;
 - (b) incubating the immobilized ligand library with one or more protein mixture;
 - (c) detecting an immobilized ligand-protein binding pair from the incubation mixture;
 - 25 (c) identifying the ligand of the ligand-binding pair; and
 - (d) identifying the protein of the ligand-binding pair;wherein the identified ligand and protein are specific members of a previously unknown ligand-protein binding pair.
- 30 3. A process for identifying specific members of a previously unknown protein-ligand binding pair, comprising the steps of:
 - (a) synthesizing a ligand library comprising small organic molecules onto resin beads to form an immobilized ligand library, wherein each bead of the immobi-
lized library comprises one member of the ligand library;
 - 35 (b) incubating the immobilized ligand library with one or more protein mixture;

(c) detecting an immobilized ligand-protein binding pair from the incubation mixture;

(d) identifying the ligand of the ligand-binding pair; and

(e) identifying the protein of the ligand-binding pair;

5 wherein the identified ligand and protein are specific members of a previously unknown ligand-protein binding pair.

4. The process according to any of claims 2 and 3, wherein the process comprises incubation with two or more differentially labeled protein mixtures.

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5. The process according to any of claims 1 and 4, wherein the step of detecting an immobilised ligand-protein binding pair comprises detecting a ligand of the library that binds differentially with the differentially labeled protein mixtures to form a differential ligand-protein binding pair.

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6. The process according to any of claims 1 and 3, wherein the resin comprises polyethylene glycol.

7. The process according to any of claims 1 and 2, wherein the library comprises small organic molecules.

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8. The process according to any of claims 1 to 3, wherein the resin is PolyEthyleneGlycol Acrylamide copolymer (PEGA), Super Permeable Organic Combinatorial Chemistry (SPOCC) or PolyOxyEthylene-PolyOxyPropylene (POEPOP) resin.

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9. The process according to any of claims 1 to 3, wherein the ligand library comprises a parallel array of random modifications of one or more ligand.

10. The process of claim 9, wherein said library comprises a parallel array of random modifications of a known compound and wherein said protein mixture comprises protein not previously known to bind said compound.

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11. The process according to any of claims 2 and 3, wherein each protein mixture is not labeled prior to incubation with the ligand library, and wherein each ligand-protein binding pair is detected after incubation by addition of a detection probe.

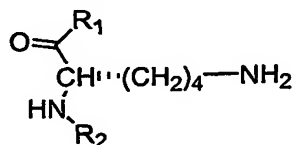
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12. The process of claim 11, wherein the detection probe is silver.
13. The process according to any of claims 1 to 3, wherein each protein mixture is la-
5 beled with a detection probe, and wherein each ligand-protein binding pair is de-
tected by detection of the probe.
14. The process of claim 13, wherein at least one detection probe produces fluorescence.
- 10 15. The process of claim 14, wherein at least one detection probe is selected from the
group consisting of Oregon Green 514, anthranilic acid, Rhodamine red, cyanine dye
2, cyanine dye 3 and cyanine dye 5.
- 15 16. The process according to any of claims 1 to 3, wherein at least one mixture of pro-
teins is a mixture of mammalian tissue cell proteins.
17. The process according to any of claims 1 to 3, wherein at least one protein mixture is
a mixture of viral proteins.
- 20 18. The process according to any of claims 1 to 3, wherein at least one protein mixture is
a mixture of bacterial proteins.
19. The process according to any of claims 1 to 3, wherein at least one protein mixture is
a mixture of mammalian proteins.
- 25 20. The process according to any of claims 1 to 3, wherein at least one protein mixture is
a mixture of human proteins.
21. The process according to any of claims 1 to 3, wherein at least one protein mixture is
30 a mixture of plant proteins.
22. The process according to any of claims 1 and 2, wherein the ligand library is a pep-
tide library.
- 35 23. The process of claim 22, wherein the ligand library comprises glycopeptides.

24. The process of claim 22, wherein the ligand library comprises lipopeptides.
- 5 25. The process of claim 22, wherein the ligand library comprises modified peptide scaffolds.
26. The process according to any of claims 1 to 3, wherein the ligand library comprises peptidomimetics.
- 10 27. The process according to any of claims 1 and 2, wherein the ligand library comprises small organic molecules.
28. The process according to any of claims 1 to 3, wherein the ligand library consists of small organic molecules.
- 15 29. The process according to any of claims 1 to 3, wherein at least one protein mixture comprises a family of proteins, and wherein the ligand- protein binding pair is detected by immunoassay.
- 20 30. The process according to any of claims 1 to 3, wherein the ligand is identified using mass spectrometry.
31. The process according to any of claims 1 to 3, wherein the ligand is identified using NMR spectroscopy.
- 25 32. The process according to any of claims 1 to 3, wherein the protein is identified using mass spectrometry.
33. The process according to any of claims 1 to 3, further comprising isolating a resin bead containing the immobilized ligand-protein binding pair from the bulk of the ligand library.
- 30 34. The process according to claim 33, wherein the steps of identifying the ligand and identifying the protein are carried out on the isolated resin bead.
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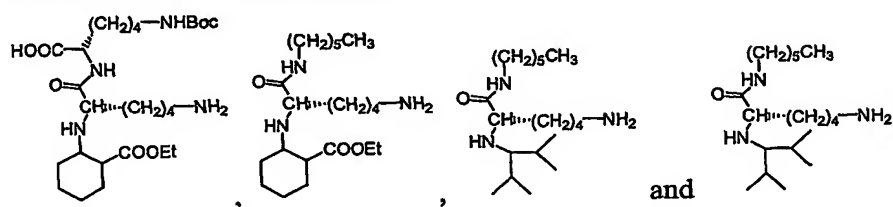
35. The process according to claim 33, wherein identifying the protein involves protease treatment of the protein on the resin bead.

36. A ligand according to formula I,



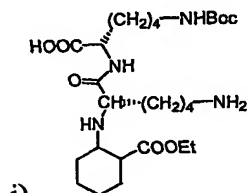
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wherein said ligand is selected from the group consisting of



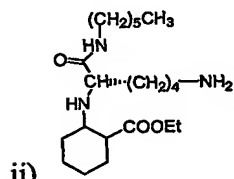
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37. An isolated ligand-protein binding pair consisting of a ligand according to claim 36 and a protein, wherein said isolated ligand-protein binding pair is selected from the group consisting of

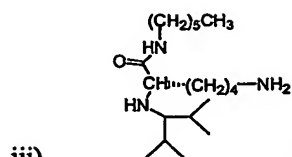


i) and (Angiotensin converting enzyme (P22967) or U2 nuclear ribonucleoprotein auxiliary factor (gi 2842676);

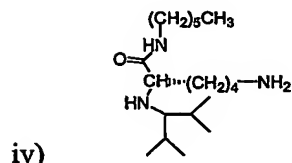
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ii) and Inward rectifier potassium channel 13 (Q9QZ65, IRKD_CAVPO); Sulfonylurea receptor 2 (Q63563); or small conductance potassium channel (P58391);

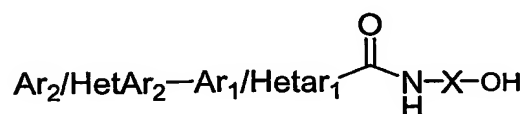


and Heat Shock protein 70kDa protein 12A (Q8KOU4);
Serine/threonine protein kinase (O88866) or Ras GTPase activating protein
2 (GAP1m) (P58069); and



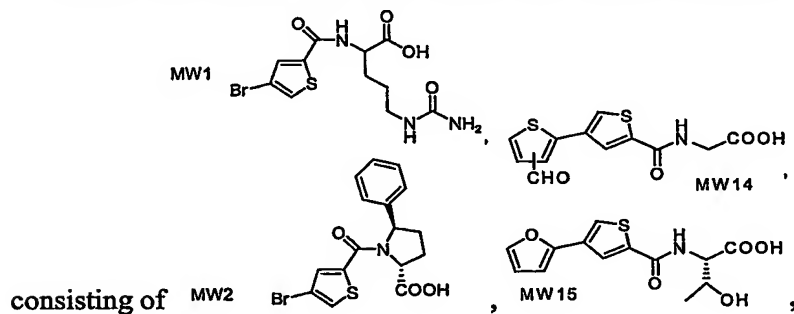
and Glycogen synthase kinase-3 beta factor (AQ9WV60).

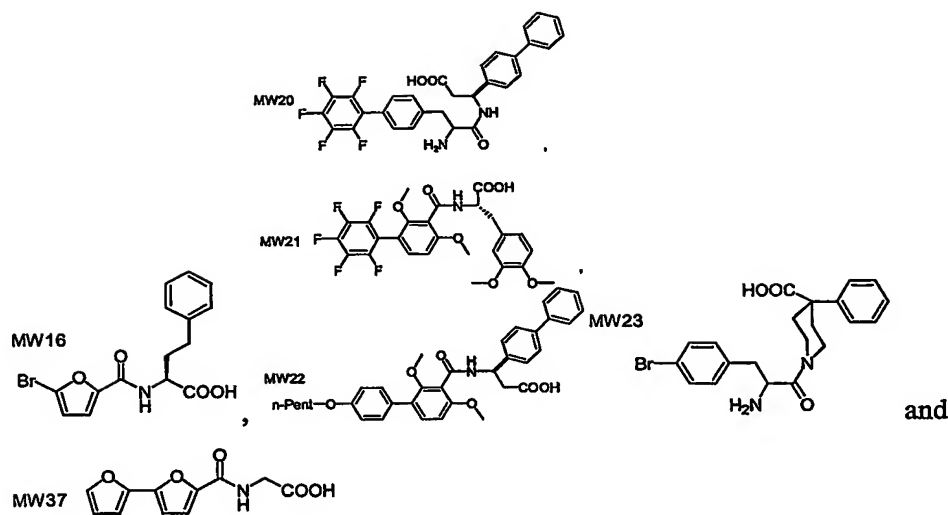
38. A ligand according to formula II



wherein X is a side chain of a compound selected from compounds 3 to 47, 64 to 75 and 106 of tables 1, 2, 3 and 7; Ar₁/Hetar₁ is selected from the group consisting of compounds 76 to 81 as indicated in table 7 and Ar₂/Hetar₂ is selected from the group consisting of compounds 82 to 101 as indicated in table 8.

39. The ligand according to claim 38, wherein said ligand is selected from the group





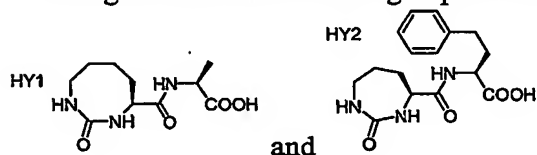
40. An isolated ligand-protein binding pairs comprising the ligand according to any of claims 38 and 39; and a protein.

41. The isolated ligand-protein binding pair according to claim 40, wherein said pair is selected from the group consisting of

- a) MW1 and (APK1 antigen (2134769) or Hyaluronan synthase 2 (gi12049586));
- b) MW2 and (APK1 antigen (2134769) or Hyaluronan synthase 2 (gi12049586));
- c) MW14 and (Unnamed protein product (26336134); Serine/threonine kinase 9/cylin dependent Serine/threonine kinase 9(23271297/4507281); Caveolin 1(gi 4972627/AAD347221) or (V) Envelope glycoprotein (gi 3832399));
- d) MW15 and (Unnamed protein product (26336134); Serine/threonine kinase 9/cylin dependent Serine/threonine kinase 9(23271297/4507281); Caveolin 1(gi 4972627/AAD347221) or (V) Envelope glycoprotein (gi 3832399));
- e) MW16 and (7 Transmembrane helix receptor (gi 21928697); DEAD (Asp-Glu-Ala-Asp) box polypeptide. (gi 19527256); 60s ribosomal protein L12 mito precursor (gi 1710600); (V) HLA-binding protein (gi 1279435) or Large subunit of ribonucleotide reductase (gi 30984467));
- f) MW20 and (Cytochrome P450 2C23 (Arachidonic acid epoxigenase) (CYP11C23, P24470); Splice isoform Calcitonin, variant displaced from P41547 Calcitonin precursor (CAL0_CANFA, P22892) or Adaptor protein complex AP-1 gamma-1 subunit with Golgi adaptor HA1/AP1 adaptin gamma-1 subunit) (P41547-00-00-00));
- g) MW21 and (Cytochrome P450 2C23 (Arachidonic acid epoxigenase) (CYP11C23, P24470); Splice isoform Calcitonin, variant displaced from P41547 Calcitonin pre-

- cursor (CAL0_CANFA, P22892) or Adaptor protein complex AP-1 gamma-1 subunit with Golgi adaptor HA1/AP1 adaptin gamma-1 subunit) (P41547-00-00-00));
- h) MW22 and (Cytochrome P450 2C23 (Arachidonic acid epoxigenase) (CYP11C23, P24470); Splice isoform Calcitonin, variant displaced from P41547 Calcitonin precursor (CAL0_CANFA, P22892) or Adaptor protein complex AP-1 gamma-1 subunit with Golgi adaptor HA1/AP1 adaptin gamma-1 subunit) (P41547-00-00-00));
- i) MW23 and (Zinc finger protein 198 (Fused in myeloproliferative disorders protein) (Q9UbW7) or Unnamed protein product (gi 12844245)); and
- j) MW37 and Serine-threonine kinase (gi 474842); Hemopexin precursor (Beta-1B-glycoprotein) (P02790) or 116 kDa U5 small nuclear ribonucleoprotein component (O08810).

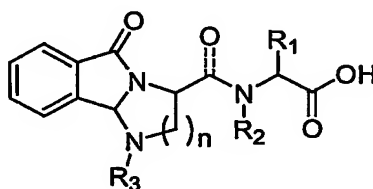
42. A ligand selected from the group consisting of



43. An isolated ligand-protein binding pair comprising a ligand according to claim 42 and a protein, wherein said pair is selected from the group consisting of

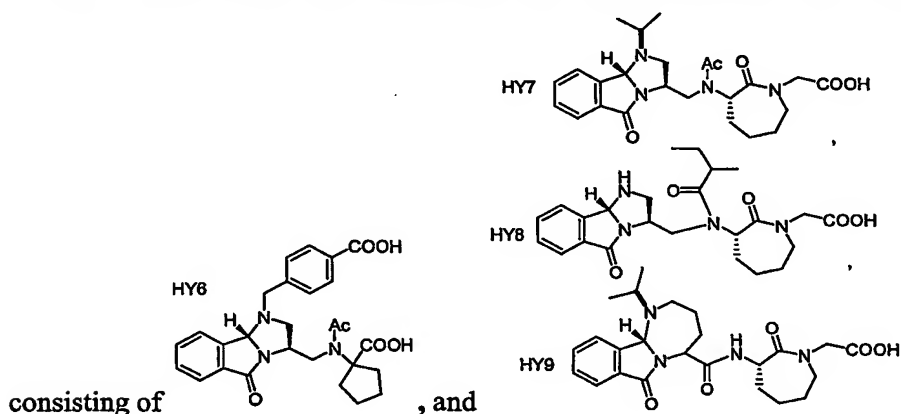
- a) HY1 and (Protein kinase C binding protein 1 also contains a zinc finger domain with protein 8) (Q9UIU4) or Guanine nucleotide-binding protein G(S), alpha subunit (Adenylate cyclase-stimulating G alpha protein) (P048949)); and
- b) HY2 and (Protein kinase byr2 (Protein kinase ste8) (MAP kinase) (P28829); Similar to protein kinase 2 (Testicular) (Q885R6) or Thiamine-triphosphatase (Q8CgV7)).

44. A ligand according to formula IV:



Wherein R_1 is the side chain of an amino acid selected from the group consisting of compound 3 to 47, 64, 66, 67, 71, 73, 74, 103 to 106 and 128 of tables 1, 2, 3, 7 and 9, R_2 is selected from the group consisting of compounds 117 to 126 as outlined in table 9 and hydrogen and R_3 is selected from the group consisting of compounds 103 to 116 and 128 of table 9.

45. The ligand according to claim 44, wherein said ligand is selected from the group



46. An isolated ligand-protein binding pair comprising a ligand according to any of claims 44 and 45; and a protein.

47. The isolated ligand-protein binding pair according to claim 46, wherein said binding pair is selected from the group consisting of:

- a) HY6 and (Myosin chain (Q63358) or NF-kappa B-repressing factor (Transcription factor ITBA4 protein) (O15226)).
- b) HY7 and (Zinc finger protein 339 (Q9BRPO) or DNA repair protein RAD52 homolog (P43351)).
- c) HY8 and (Zinc finger protein 339 (Q9BRPO) or DNA repair protein RAD52 homolog (P43351)).
- d) HY9 and Zinc finger protein 339 (Q9BRPO) or DNA repair protein RAD52 homolog (P43351).

48. A ligand comprising or consisting of Pya-Hyp-Hyp-Phe-Acm-Tyr [SEQ ID NO: 8].

49. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 48; and
- b) Troponin T, Growth hormone receptor, or Protein kinase.

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50. A ligand comprising or consisting His-Tyr-Pip-Thr-Acm-Abi [SEQ ID NO: 14];

51. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 50; and
- b) Chain C P27 cyclin A-CDK2 complex: (Cyclin A?) (gi2392395); Hypothetical protein XP_154035.

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52. A ligand comprising or consisting of Phe-Thr-Pya-Pip-Asp-His [SEQ ID NO: 11].

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53. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 52; and
- b) Sodium channel (gi 18591322) (M); Chloride channel (gi 6978663/4502867) (M); Troponin I (gi 1351298); Zn Finger protein (gi 18591322) (MA); SPTR (peroxisomal Ca dependent solute carrier (putative) (gi 12853685); Beta-2 ad-
nergic receptor (gi 12699028)

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54. A ligand comprising or consisting of Phe-Abi-Pal-Hyp-Thr-Hyp [SEQ ID NO: 65].

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55. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 54; and
- b) Zinc finger associated protein, Ribosomal proteins, or Protein phosphatase.

56. A ligand comprising or consisting of Phe-Gua-Pal-Tyr-Gua-Tyr [SEQ ID NO: 66].

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57. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 56; and
- b) Glucose-6-Phosphatase, Succinate dehydrogenase, ARL-interacting protein, SPTR, or Nucleic acid binding protein.

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58. A ligand comprising or consisting of Abi-Thr-Hyp-Hyp-His-- [SEQ ID NO: 67].
59. An isolated ligand-protein binding pair comprising:
- a) The ligand according to claim 58; and
 - b) Phosphofructokinase, Selenium binding protein, Serine arginine rich protein kinase, Guanylate kinase, Protein tyrosine kinase, Alkaline phosphatase, Symporter, SPTR, WAP-protein, GTP Hydrolase, or Actin filament.
60. A ligand comprising or consisting of Pya-Gua-Abi-Asp-Abi-Tyr [SEQ ID NO: 69].
61. An isolated ligand-protein binding pair comprising:
- a) The ligand according to claim 60; and
 - b) SPTR (gi 20869775) (M); Ribosomal proteins (60s) (gi 20875941/6677773); (Calcium channel (gi 3202010) (M); Slo channel protein isoform (gi 3644046) (M); Potassium conductance calcium activated channel (gi 6754436,NP_034740) (M); ; Regulator of G-protein signalling 8 (gi 9507049). .
62. A ligand comprising or consisting of Abi-Phe-Abi-Phe-Che-Tyr [SEQ ID NO: 18].
63. An isolated ligand-protein binding pair comprising:
- a) The ligand according to claim 62; and
 - b) Cathepsin E, Ribosomal protein, Actin binding protein, or Amino acid transferase.
64. A ligand comprising or consisting of Pal-Gly-Abi-Hyp-Pya-Trp [SEQ ID NO: 56]
65. An isolated ligand-protein binding pair comprising:
- a) The ligand according to claim 64; and
 - b) NAS putative unclassified (gi 12861084); Putative Zn finger protein 64 (gi 12849329).
66. A ligand comprising or consisting of T(Sa)-F-G-I-W [SEQ ID NO: 21].
67. An isolated ligand-protein binding pair comprising:
- a) The ligand according to claim 66; and

b) Histidine synthetase or aspartate carbamoyl transferase.

68. A ligand comprising or consisting of T(Sa)-G-V-F-L [SEQ ID NO: 23].

5 69. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 68; and
- b) 50 S ribosomal protein, heme binding lipoprotein, regulator for D-glucarate, D-glycerate and D-galactarate, or glutamine tRNA synthetase.

10 70. A ligand comprising or consisting of T(Sa)-H-W-V-V [SEQ ID NO: 27].

71. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 70; and
- b) Pyruvoyl dependent aspartate decarboxylase, colicin E2, or Histidine kinase.

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72. A ligand comprising or consisting of T(Sa)-H-L-G-Y [SEQ ID NO: 28].

73. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 72; and
- b) phosphomannose isomerase.

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74. A ligand comprising or consisting of T(Sa)-M-V-N-W [SEQ ID NO: 32].

75. An isolated ligand-protein binding pair comprising:

- 25 a) The ligand according to claim 74; and
- b) ATP dependent helicase or mob C.

76. A ligand comprising or consisting of T(Sa)-H-W-H-L [SEQ ID NO: 35].

30 77. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 76; and
- b) Chorismate mutase, xanthine dehydrogenase, or carbamoyl phosphate synthetase.

78. A ligand comprising or consisting of T(Sa)-Q-P-G-M [SEQ ID NO: 63]

79. An isolated ligand-protein binding pair comprising:

- 5 a) The ligand according to claim 78; and
 b) ATP dependent helicase: HrpA homolog (NCBIBAA15034); Putative protease ydcP precursor (NCBI P76104)..

80. A ligand comprising or consisting of Gly-Pro-Lys-Lys-Tyr-His [SEQ ID NO: 44].

10 81. An isolated ligand-protein binding pair comprising:

- a) The ligand according to claim 80; and
 b) Con A, *P. sativum* lectin, or *L. culinaris* lectin.

15 82. Use of a protein selected from the group consisting of Sodium channel (gi 18591322) Chloride channel (gi 6978663/4502867); Zn Finger protein (gi 18591322) SPTR (peroxisomal Ca dependent solute carrier (putative) (gi 12853685); Beta-2 adrenergic receptor (gi 12699028), Zinc finger associated protein (gi 20304091); Glucose-6-Phosphatase (gi 6679893/15488608), Succinate dehydroge-
20 nase, ARL-interacting protein (gi 4927202); Nucleic acid binding protein; Phospho-
fructokinase (gi 7331123), Selenium binding protein (gi 8848341/6677907), Serine
arginine rich protein kinase; Guanylate kinase (gi 20986250), Calcium channel (gi
3202010 Slo channel protein isoform (gi 3644046) Potassium conductance calcium
activated channel (gi 6754436, NP_034740) Regulator of G-protein signalling 8 (gi
9507049); Regulator of G-protein signalling 14, Cathepsin E (gi 4503145), Putative
25 Zn finger protein 64 (gi 12849329); Histidine synthetase (gi 15803037); aspartate
carbamoyl transferase (pyrI_E.coli); 50 S ribosomal protein; heme binding lipopro-
tein (gi 4062402/40624079) glutamine tRNA synthetase (gi 146168); Pyruvoyl de-
pendent aspartate decarboxylase (gi 3212459), Histidine kinase (part belongs to
narQ_E.coli); phosphomannose isomerase (gi 147164); ATP dependent helicase (gi
30 2507332/16128141); mob C (gi 78702); Chorismate mutase (gi 1800006), car-
bamoyl phosphate synthetase (carB_E.coli); ATP dependent helicase: HrpA ho-
molog (NCBIBAA15034); Inward rectifier potassium channel 13 (Q9QZ65,
IRKD_CAVPO); Sulfonylurea receptor 2 (Q63563); small conductance potassium
channel (P58391), Serine/threonine protein kinase (O88866); Ras GTPase activating
35 protein 2 (GAP1m) (P58069), Glycogen synthase kinase-3 beta factor (AQ9WV60),

Serine/threonine kinase 9/cylin dependent Serine/threonine kinase 9(23271297/4507281); NF-kappa B-repressing factor (Transcription factor ITBA4 protein) (O15226), HLA-binding protein (gi 1279435) and Large subunit of ribonucleotide reductase (gi 30984467) as drug target, in a method to identify one or more drugs for the treatment of a clinical condition.

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83. Use according to claim 82, wherein the protein is selected from the group consisting of Chaperone DnaK (dnak_E.coli), Histidine synthetase (gi 15803037), aspartate carbamoyl transferase (pyrI_E. coli), glutamine tRNA synthetase (gi146168). tyrosine protein kinase (gi 20140365), citrate synthetase (CISY_E.coli), Pyruvoyl dependent aspartate decarboxylase (gi 3212459), colicin E2. (gi809671/809683), Histidine kinase (part belongs to narQ_E.coli), Protein involved in lipopolysaccharide biosynthesis (gi 16131496), phosphomannose isomerase (gi147164), high affinity potassium transport system (kdpC_E.coli), ATP dependent helicase (gi 2507332/16128141), mob C (gi 78702); Orf hypothetical protein (yciL_E.coli), outer membrane pyruvate kinase (gi16129807/15831818), alkaline phosphatase, , Chorismate mutase (gi 1800006), carbamoyl phosphate synthetase (carB_E.coli); Glutamate synthase (NaDPH) (gi 2121143), protein involved in flagellar biosynthesis and motor switching component,), Serine tRNA synthetase (gi15830232) and ATP dependent helicase: HrpA homolog (NCBIBAA15034).

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84. Use according to claim 82, wherein the protein is selected from the group consisting of transposase, proteins involved in Chaperone DnaK (dnak_E.coli), transposase (gi 158316821), Histidine synthetase (gi 15803037), aspartate carbamoyl transferase (pyrI_E. coli), transcriptional regulator (gi 18265863 glutamine tRNA synthetase (gi146168). tyrosine protein kinase (gi 20140365), citrate synthetase (CISY_E.coli), Pyruvoyl dependent aspartate decarboxylase (gi 3212459), Histidine kinase (part belongs to narQ_E.coli), Protein involved in lipopolysaccharide biosynthesis (gi 16131496), phosphomannose isomerase (gi147164), ATP dependent helicase (gi 2507332/16128141), Chorismate mutase (gi 1800006), carbamoyl phosphate synthetase (carB_E.coli); Glutamate synthase (NaDPH) (gi 2121143), Serine tRNA synthetase (gi15830232), ATP dependent helicase: HrpA homolog (NCBI-BAA15034), HLA-binding protein (gi 1279435); Large subunit of ribonucleotide reductase (gi 30984467)

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85. Use according to any of claims 83 and 84, wherein the clinical condition is an infection.

86. Use according to claim 82, wherein the protein is selected from the group consisting of Ca²⁺/Calmodulin activated Myosin light chain kinase (gi 284660), Regulator of G-Protein Signalling (RGS14) variant (gi 2708808), SPTR (gi 20837095), Sodium channel (gi 18591322); Chloride channel (gi 6978663/4502867); Zn Finger protein (gi 18591322); SPTR (peroxisomal Ca dependent solute carrier (putative) (gi 12853685); Beta-2 adnergic receptor (gi 12699028); Serine/threonine Protein kinase (gi 5730055); Chain C P27 cyclin A-CDK2 complex: (Cyclin A?) (gi2392395); Membrane spanning 4-domain subfamily A member II (gi7435941); Zinc finger associated protein (gi 20304091); Serine arginine rich protein kinase; SPTR (gi 20869775); Calcium channel (gi 3202010); Slo channel protein isoform (gi 3644046); Potassium conductance calcium activated channel (gi 6754436,NP_034740); ; Regulator of G-protein signalling 8 (gi 9507049); Cathepsin E (gi 4503145); NAS putative unclassified (gi 12861084); Putative Zn finger protein 64 (gi 12849329); Cell surface glycoprotein (gi 23603627); Hypothetical protein (XP-179829; gi 14720727); Orphan Nuclear receptor similar to hsp40 (NRID 26166582, Inward rectifier potassium channel 13 (Q9QZ65, IRKD_CAVPO); Sulfonylurea receptor 2 (Q63563); small conductance potassium channel (P58391), Serine/threonine protein kinase (O88866); Ras GTPase activating protein 2 (GAP1m) (P58069), Glycogen synthase kinase-3 beta factor (AQ9WV60), Serine/threonine kinase 9/cylin dependent Serine/threonine kinase 9(23271297/4507281); NF-kappa B-repressing factor (Transcription factor ITBA4 protein) (O15226),.

87. Use according to claim 82, wherein the protein is selected from the group consisting of Ca²⁺/Calmodulin activated Myosin light chain kinase (gi 284660), Regulator of G-Protein Signalling (RGS14) variant (gi 2708808), SPTR (gi 20837095), Zn Finger protein (gi 18591322); SPTR (peroxisomal Ca dependent solute carrier (putative) (gi 12853685); Beta-2 adrenergic receptor (gi 12699028); Serine/threonine Protein kinase (gi 5730055); Chain C P27 cyclin A-CDK2 complex: (Cyclin A?) (gi2392395); Zinc finger associated protein (gi 20304091); Serine arginine rich protein kinase; SPTR (gi 20869775); Regulator of G-protein signalling 8 (gi 9507049); Cathepsin E (gi 4503145); Putative Zn finger protein 64 (gi 12849329); Orphan Nuclear receptor

5 similar to hsp40 (NRID 26166582), Inward rectifier potassium channel 13 (Q9QZ65, IRKD_CAVPO); small conductance potassium channel (P58391), Serine/threonine protein kinase (O88866); Ras GTPase activating protein 2 (GAP1m) (P58069), Glycogen synthase kinase-3 beta factor (AQ9WV60), Serine/threonine kinase 9/cylin dependent Serine/threonine kinase 9(23271297/4507281); NF-kappa B-repressing factor (Transcription factor ITBA4 protein) (O15226),

88. Use according to any of claims 86 and 87, wherein the clinical condition is a cardiovascular disease.